

SECRET

85

<210> 6
<211> 15
<212> DNA
<213> primer

<400> 6
ggggs ggggs ggggs

15

<210> 7
<211> 35
<212> DNA
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<400> 7
gcggcccagc cggcccaggt gcagctggtg cagag

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<210> 8
<211> 34
<212> DNA
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ctgcggccgc ttgatctcc accttggtgc cctg

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<210> 9
<211> 38
<212> DNA
<213> primer

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tcccaagctt tcaccatgca ggtgcagctg gtgcagag

38

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cccgtcgcag tcatttgatc tccaccttgg tgc

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<400> 11
tcccagatct aagcttgccg ccaccatgga ctgg

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<213> primer

<400> 12
gctgatctcg cccacccact cc

22

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<210> 13
<211> 30
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<400> 13
cccgagatct cgagtcattt gatctccacc

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<210> 14
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ggagatctcc acagtccttg aacacac

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<400> 15
tcatttacct ggagacaggg a

21

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<400> 16
ctaactctt cccctgttga a

21

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<212> DNA
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<400> 17
tgaagaaagc ttgccgccac catggag

27

<210> 18

<212> DNA
<213> primer

<400> 18
gcacccgctc gtttgatctc caccttggt

29

<210> 19
<211> 38
<212> DNA
<213> primer

<400> 19
cggaattcga gcggatgctg caccaactgt atcgatct

38

<210> 20

0909147613091

40

21

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<212> DNA
<213> human/murine
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<221> CDS
<222> (1) ... (366)
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cag gtg cag ctg gtg cag agc ggc gcc gag gtg aag aag ccc ggc gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

agc gtg aag gtg agc tgc aag gcc agc ggc tac acc ttc agc atg tac 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Met Tyr
 20 25 30

tgg ctg gag tgg gtg agg cag gcc ccc ggc cac ggc ctg gag tgg gtg 144
Trp Leu Glu Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu Trp Val
35 40 45

ggc gag atc agc ccc ggc acc ttc acc acc aac tac aac gag aag ttc 192
Gly Glu Ile Ser Pro Gly Thr Phe Thr Thr Asn Tyr Asn Glu Lys Phe
50 . 55 60

Lys Ala Arg Ala Thr Phe Thr Ala Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

atg	gag	ctg	agc	agc	ctg	agg	agc	gag	gac	acc	gcc	gtg	tac	tac	tgc	288
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			

gcc agg ttc agc cac ttc agc ggc agc aac tac gac tac ttc gac tac 336
Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

tgg ggc cag ggc acc ctg gtg acc gtg agc tca 369
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120

SECRET

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Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ser	Met	Tyr
			20					25					30		
Trp	Leu	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	His	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Glu	Ile	Ser	Pro	Gly	Thr	Phe	Thr	Thr	Asn	Tyr	Asn	Glu	Lys	Phe
	50					55				60					

Lys	Ala	Arg	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Phe	Ser	His	Phe	Ser	Gly	Ser	Asn	Tyr	Asp	Tyr	Phe	Asp	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser						
		115					120								

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<221> CDS
<222> (1) ... (321)
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1 5 10 15

gag agg gcc acc ctg agc tgc agg gcc agc cag agc atc ggc acc aac 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30

atc cac tgg tac cag cag aag ccc ggc cag gcc ccc agg ctg ctg atc 144
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

aag tac gcc agc gag agc atc agc ggc atc ccc agc agg ttc agc ggc 192
Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

agc ggc agc ggc acc gac ttc acc ctg acc atc agc agg ctg gag ccc 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
 65 70 75 80

gag gac ttc gcc atg tac tac tgc cag cag agc gac agc tgg ccc acc 288
Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln Ser Asp Ser Trp Pro Thr
85 90 95

321

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Asp	Ile	Leu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1				5					10					15		
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	
			20					25					30			
Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	
		35				40						45				
Lys	Tyr	Ala	Ser	Glu	Ser	Ile	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	
65					70					75				80		
Glu	Asp	Phe	Ala	Met	Tyr	Tyr	Cys	Gln	Gln	Ser	Asp	Ser	Trp	Pro	Thr	
				85					90					95		
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105								

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<220>  
<221> CDS  
<222> (1) ... (735)
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48

144

192

240

atg gag ctg agc agc ctg agg agc gag gac acc gcc gtg tac tac tgc 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcc agg ttc agc cac ttc agc ggc agc aac tac gac tac ttc gac tac 336
Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

tgg ggc cag ggc acc ctg gtg acc gtg agc tca ggt ggc ggt ggc tgc 384
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

ggc ggt ggt ggg tgc ggt ggc ggc gga tct gac atc ctg ctg acc cag 432
Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Leu Leu Thr Gln
130 135 140

agc ccc ggc acc ctg agc ctg agc ccc ggc gag agg gcc acc ctg agc 480
Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
145 150 155 160

tgc agg gcc agc cag agc atc ggc acc aac atc cac tgg tac cag cag 528
Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln
165 170 175

aag ccc ggc cag gcc ccc agg ctg ctg atc aag tac gcc agc gag agc 576
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser
180 185 190

atc agc ggc atc ccc agc agg ttc agc ggc agc ggc agc ggc acc gac 624
Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

ttc acc ctg acc atc agc agg ctg gag ccc gag gac ttc gcc atg tac 672
Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Met Tyr
210 215 220

tac tgc cag cag agc gac agc tgg ccc acc acc ttc ggc cag ggc acc 720
Tyr Cys Gln Gln Ser Asp Ser Trp Pro Thr Phe Gly Gln Gly Thr
225 230 235 240

Lys Val Glu Ile Lys 735
245

<210> 27

<211> 245

<212> PRT

<213> human/murine

<400> 27

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Met Tyr
20 25 30
Trp Leu Glu Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu Trp Val
35 40 45

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Gly	Glu	Ile	Ser	Pro	Gly	Thr	Phe	Thr	Thr	Asn	Tyr	Asn	Glu	Lys	Phe
50						55					60				
Lys	Ala	Arg	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Phe	Ser	His	Phe	Ser	Gly	Ser	Asn	Tyr	Asp	Tyr	Phe	Asp	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
		115					120					125			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Leu	Leu	Thr	Gln
		130				135					140				
Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser
145					150					155					160
Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	Ile	His	Trp	Tyr	Gln	Gln
				165					170					175	
Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Lys	Tyr	Ala	Ser	Glu	Ser
			180					185					190		
Ile	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
		195					200					205			
Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Met	Tyr
		210				215					220				
Tyr	Cys	Gln	Gln	Ser	Asp	Ser	Trp	Pro	Thr	Thr	Phe	Gly	Gln	Gly	Thr
225					230					235					240
Lys	Val	Glu	Ile	Lys											
				245											

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